

SEQUENCE SUBMISSION

SEQ ID NO: 1 provides primate IL-1 δ nucleotide sequence.
SEQ ID NO: 2 provides priamte IL-1 δ polypeptide sequence.
5 SEQ ID NO: 3 provides primate IL-1 ϵ nucleotide sequence.
SEQ ID NO: 4 provides primate IL-1 ϵ polypeptide sequence.
SEQ ID NO: 5 provides primate IL-1 α polypeptide sequence.
SEQ ID NO: 6 provides primate IL-1 β polypeptide sequence.
SEQ ID NO: 7 provides primate IL-1RA polypeptide sequence.
10 SEQ ID NO: 8 provides rodent IL-1 γ (IGIF) polypeptide sequence.
SEQ ID NO: 9 provides primate IL-1 γ (IGIF) polypeptide sequence.
SEQ ID NO: 10 provides rodent IL-1 ϵ polypeptide sequence.
SEQ ID NO: 11 provides rodent IL-1 δ polypeptide sequence.
15 SEQ ID NO: 12 provides primate IL-1R6 nucleotide sequence.
SEQ ID NO: 13 provides primate IL-1R6 polypeptide sequence.
SEQ ID NO: 14 provides rodent IL-1R6 nucleotide sequence.
SEQ ID NO: 15 provides rodent IL-1R6 polypeptide sequence.

20 <110> Debets, Johannes E.M.A.
Timans, Jacqueline C.
Bazan, J. Fernando
Kastelein, Robert A.

25 <120> Mammalian Cytokines; Receptors; Related Reagents and
Methods

<130> DX01073P

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35 <170> PatentIn Ver. 2.1

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Homo sapiens

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55 1 5 10 15

aag gtg ctt tat ctg cat aat aac cag ctt cta gct gga ggg ctg cat 105
Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His
20 25 30

60 153

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5	tgg ctg gat gcc agc ctg tcc ccc gtc atc ctg ggt gtc cag ggt gga Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly 50 55 60	249
10	agc cag tgc ctg tca tgt ggg gtg ggg cag gag ccg act cta aca cta Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu 65 70 75 80	297
15	gag cca gtg aac atc atg gag ctc tat ctt ggt gcc aag gaa tcc aag Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys 85 90 95	345
20	agc ttc acc ttc tac cgg cgg gac atg ggg ctc acc tcc agc ttc gag Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu 100 105 110	393
	tcg gct gcc tac ccg ggc tgg ttc ctg tgc acg gtg cct gaa gcc gat Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp 115 120 125	441
25	cag cct gtc aga ctc acc cag ctt ccc gag aat ggt ggc tgg aat gcc Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala 130 135 140	489
30	ccc atc aca gac ttc tac ttc cag cag tgt gac tagggcaacg tgccccccag 542 Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp 145 150 155	
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	Homo sapiens	
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5 Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg
35 40 45

Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
10 50 55 60

Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
65 70 75 80

Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys
15 85 90 95

Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu
100 105 110

Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp
20 115 120 125

Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Trp Asn Ala
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Homo sapiens

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<222> (67)..(573)

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Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Arg Ala
1 5 10

50 gtc tat caa tca atg tgt aaa cct att act ggg act att aat gat ttg 156
Val Tyr Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu
15 20 25 30

55 aat cag caa gtg tgg acc ctt cag ggt cag aac ctt gtg gca gtt cca 204
Asn Gln Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro
35 40 45

60 cga agt gac agt gtg acc cca gtc act gtt gct gtt atc aca tgc aag 252
Arg Ser Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys
50 55 60

tat cca gag gct ctt gag caa ggc aga ggg gat ccc att tat ttg gga 300
 Tyr Pro Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly
 65 70 75
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 atc cag aat cca gaa atg tgt ttg tat tgt gag aag gtt gga gaa cag 348
 Ile Gln Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln
 80 85 90
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 ccc aca ttg cag cta aaa gag cag aag atc atg gat ctg tat ggc caa 396
 Pro Thr Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln
 95 100 105 110
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 ccc gag ccc gtg aaa ccc ttc ctt ttc tac cgt gcc aag act ggt agg 444
 Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg
 115 120 125
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 acc tcc acc ctt gag tct gtg gcc ttc ccg gac tgg ttc att gcc tcc 492
 Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser
 130 135 140
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 tcc aag aga gac cag ccc atc att ctg act tca gaa ctt ggg aag tca 540
 Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser
 145 150 155
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 tac aac act gcc ttt gaa tta aat ata aat gac tgaactcagc ctagaggtgg 593
 Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp
 160 165
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 cagcttggtc tttgtcttaa agtttctggc tcccaatgtg tttcgtctc cattttctta 653
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 gaagatgctt cagagctcat gcgcgttacc cacgatggca tgactagcac agagctgatc 953
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 Homo sapiens
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35 40 45

Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro
50 55 60

5 Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
65 70 75 80

Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
10 85 90 95

Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
100 105 110

15 Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
115 120 125

Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
130 135 140

20 Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn
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Homo sapiens

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Ser Ile Ile Arg Ala Asn Asp Gln Tyr Leu Thr Ala Ala Ala Leu His
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45 Asn Leu Asp Glu Ala Val Lys Phe Asp Met Gly Ala Tyr Lys Ser Ser
35 40 45

Lys Asp Asp Ala Lys Ile Thr Val Ile Leu Arg Ile Ser Lys Thr Gln
50 55 60

50 Leu Tyr Val Thr Ala Gln Asp Glu Asp Gln Pro Val Leu Leu Lys Glu
65 70 75 80

55 Met Pro Glu Ile Pro Lys Thr Ile Thr Gly Ser Glu Thr Asn Leu Leu
85 90 95

Phe Phe Trp Glu Thr His Gly Thr Lys Asn Tyr Phe Thr Ser Val Ala
100 105 110

60 His Pro Asn Leu Phe Ile Ala Thr Lys Gln Asp Tyr Trp Val Cys Leu
115 120 125

Ala Gly Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Asn Gln
130 135 140

5 Ala
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Homo sapiens

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Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala Leu His Leu Gln
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25 Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val Gln
35 40 45

Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu Gly Leu Lys Glu
50 55 60

30 Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp Lys Pro Thr Leu
65 70 75 80

35 Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys Lys Lys Met Glu
85 90 95

Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe
100 105 110

40 Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu
115 120 125

Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gln Asp Ile Thr
130 135 140

45 Asp Phe Thr Met Gln Phe Val Ser Ser
145 150

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Homo sapiens

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Thr Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly
20 25 30

5 Pro Asn Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu Pro
35 40 45

His Ala Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser Cys
10 50 55 60

Val Lys Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Ala Val Asn Ile
65 70 75 80

15 Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile
85 90 95

Arg Ser Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro
100 105 110

20 Gly Trp Phe Leu Cys Thr Ala Met Glu Ala Asp Gln Pro Val Ser Leu
115 120 125

25 Thr Asn Met Pro Asp Glu Gly Val Met Val Thr Lys Phe Tyr Phe Gln
130 135 140

Glu Asp Glu
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Mus sp.

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Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met
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Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile
35 40 45

Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser
50 50 55 60

Val Lys Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile
65 70 75 80

55 Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser
85 90 95

Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu
100 105 110

60 Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu

115 120 125

Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
130 135 140

5 Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
145 150 155

10 <210> 9
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Homo sapiens

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Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
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25 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
35 40 45

30 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
50 55 60

35 Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile
65 70 75 80

40 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
85 90 95

Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
100 105 110

45 Met Gln Phe Glu Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
115 120 125

Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
45 130 135 140

Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
145 150 155

50 <210> 10
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<212> PRT
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55 <220>
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Mus sp.

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5	Pro Arg Lys Glu Gln Thr Val Pro Val Thr Ile Thr Leu Leu Pro Cys			
35	40	45		
10	Gln Tyr Leu Asp Thr Leu Glu Thr Asn Arg Gly Asp Pro Thr Tyr Met			
50	55	60		
15	Gly Val Gln Arg Pro Met Ser Cys Leu Phe Cys Thr Lys Asp Gly Glu			
65	70	75	80	
20	Gln Pro Val Leu Gln Leu Gly Glu Gly Asn Ile Met Glu Met Tyr Asn			
85	90	95		
25	Lys Lys Glu Pro Val Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly			
100	105	110		
30	Thr Thr Ser Thr Phe Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala			
115	120	125		
35	Val Cys Ser Lys Gly Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly			
130	135	140		
40	Glu Ile Phe Ile Thr Asp Phe Glu Met Ile Val Val His			
145	150	155		
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Mus sp.				
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65	Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Ala			
35	40	45		
70	Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly Ser			
50	55	60		
75	Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys Leu Glu			
65	70	75	80	
80	Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys Ser			
85	90	95		
85	Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu Ser			
100	105	110		

	Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala Asp Gln			
	115	120	125	
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30	gtc aca gca gat gga tgc aag gac att ttt atg aaa aat gag ata ctt		96	
	Val Thr Ala Asp Gly Cys Lys Asp Ile Phe Met Lys Asn Glu Ile Leu			
	20	25	30	
35	tca gca agc cag cct ttt gct ttt aat tgt aca ttc cct ccc ata aca		144	
	Ser Ala Ser Gln Pro Phe Ala Phe Asn Cys Thr Phe Pro Pro Ile Thr			
	35	40	45	
40	tct ggg gaa gtc agt gta aca tgg tat aaa aat tct agc aaa atc cca		192	
	Ser Gly Glu Val Ser Val Thr Trp Tyr Lys Asn Ser Ser Lys Ile Pro			
	50	55	60	
45	gtg tcc aaa atc ata cag tct aga att cac cag gac gag act tgg att		240	
	Val Ser Lys Ile Ile Gln Ser Arg Ile His Gln Asp Glu Thr Trp Ile			
	65	70	75	80
50	ttg ttt ctc ccc atg gaa tgg ggg gac tca gga gtc tac caa tgt gtt		288	
	Leu Phe Leu Pro Met Glu Trp Gly Asp Ser Gly Val Tyr Gln Cys Val			
	85	90	95	
55	ata aag ggt aga gac agc tgt cat aga ata cat gta aac cta act gtt		336	
	Ile Lys Gly Arg Asp Ser Cys His Arg Ile His Val Asn Leu Thr Val			
	100	105	110	
60	ttt gaa aaa cat tgg tgt gac act tcc ata ggt ggt tta cca aat tta		384	
	Phe Glu Lys His Trp Cys Asp Thr Ser Ile Gly Gly Leu Pro Asn Leu			
	115	120	125	
	tca gat gag tac aag caa ata tta cat ctt gga aaa gat gat agt ctc		432	
	Ser Asp Glu Tyr Lys Gln Ile Leu His Leu Gly Lys Asp Asp Ser Leu			
	130	135	140	
	aca tgt cat ctg cac ttc ccg aag agt tgt gtt ttg ggt cca ata aag		480	

	Thr Cys His Leu His Phe Pro Lys Ser Cys Val Leu Gly Pro Ile Lys		
	145 150 155 160		
5	tgg tat aag gac tgt aac gag att aaa ggg gag cggttc act gtt ttg Trp Tyr Lys Asp Cys Asn Glu Ile Lys Gly Glu Arg Phe Thr Val Leu	165 170 175	528
10	gaa acc agg ctt ttg gtg agc aat gtc tcg gca gag gac aga ggg aac Glu Thr Arg Leu Leu Val Ser Asn Val Ser Ala Glu Asp Arg Gly Asn	180 185 190	576
15	tac gcg tgt caa gcc ata ctg aca cac tca ggg aag cag tac gag gtt Tyr Ala Cys Gln Ala Ile Leu Thr His Ser Gly Lys Gln Tyr Glu Val	195 200 205	624
20	tta aat ggc atc act gtg agc att aca gaa aga gct gga tat gga gga Leu Asn Gly Ile Thr Val Ser Ile Thr Glu Arg Ala Gly Tyr Gly Gly	210 215 220	672
25	agt gtc cct aaa atc att tat cca aaa aat cat tca att gaa gta cag Ser Val Pro Lys Ile Ile Tyr Pro Lys Asn His Ser Ile Glu Val Gln	225 230 235 240	720
30	ctt ggt acc act ctg att gtg gac tgc aat gta aca gac acc aag gat Leu Gly Thr Thr Leu Ile Val Asp Cys Asn Val Thr Asp Thr Lys Asp	245 250 255	768
35	aat aca aat cta cga tgc tgg aga gtc aat aac act ttg gtg gat gat Asn Thr Asn Leu Arg Cys Trp Arg Val Asn Asn Thr Leu Val Asp Asp	260 265 270	816
40	tac tat gat gaa tcc aaa cga atc aga gaa ggg gtg gaa acc cat gtc Tyr Tyr Asp Glu Ser Lys Arg Ile Arg Glu Gly Val Glu Thr His Val	275 280 285	864
45	tct ttt cgg gaa cat aat ttg tac aca gta aac atc acc ttc ttg gaa Ser Phe Arg Glu His Asn Leu Tyr Thr Val Asn Ile Thr Phe Leu Glu	290 295 300	912
50	gtg aaa atg gaa gat tat ggc ctt cct ttc atg tgc cac gct gga gtg Val Lys Met Glu Asp Tyr Gly Leu Pro Phe Met Cys His Ala Gly Val	305 310 315 320	960
55	tcc aca gca tac att ata tta cag ctc cca gct ccg gat ttt cga gct Ser Thr Ala Tyr Ile Ile Leu Gln Leu Pro Ala Pro Asp Phe Arg Ala	325 330 335	1008
60	tac ttg ata gga ggg ctt atc gcc ttg gtg gct gtg gct gtg tct gtt Tyr Leu Ile Gly Gly Leu Ile Ala Leu Val Ala Val Ala Val Ser Val	340 345 350	1056
	gtg tac ata tac aac att ttt aag atc gac att gtt ctt tgg tat cga Val Tyr Ile Tyr Asn Ile Phe Lys Ile Asp Ile Val Leu Trp Tyr Arg	355 360 365	1104
	agt gcc ttc cat tct aca gag acc ata gta gat ggg aag ctg tat gac Ser Ala Phe His Ser Thr Glu Thr Ile Val Asp Gly Lys Leu Tyr Asp	370 375 380	1152
	gcc tat gtc tta tac ccc aag ccc cac aag gaa agc cag agg cat gcc Ala Tyr Val Leu Tyr Pro Lys Pro His Lys Glu Ser Gln Arg His Ala		1200

	385	390	395	400	
	gtg gat gcc ctg gtg ttg aat atc ctg ccc gag gtg ttg gag aga caa				1248
5	Val Asp Ala Leu Val Leu Asn Ile Leu Pro Glu Val Leu Glu Arg Gln				
	405		410	415	
	tgt gga tat aag ttg ttt ata ttc ggc aga gat gaa ttc cct gga caa				1296
	Cys Gly Tyr Lys Leu Phe Ile Phe Gly Arg Asp Glu Phe Pro Gly Gln				
	420		425	430	
10	gcc gtg gcc aat gtc atc gat gaa aac gtt aag ctg tgc agg agg ctg				1344
	Ala Val Ala Asn Val Ile Asp Glu Asn Val Lys Leu Cys Arg Arg Leu				
	435		440	445	
15	att gtc att gtg gtc ccc gaa tcg ctg ggc ttt ggc ctg ttg aag aac				1392
	Ile Val Ile Val Val Pro Glu Ser Leu Gly Phe Gly Leu Leu Lys Asn				
	450		455	460	
20	ctg tca gaa gaa caa atc gcg gtc tac agt gcc ctg atc cag gac ggg				1440
	Leu Ser Glu Glu Gln Ile Ala Val Tyr Ser Ala Leu Ile Gln Asp Gly				
	465		470	475	480
25	atg aag gtt att ctc att gag ctg gag aaa atc gag gac tac aca gtc				1488
	Met Lys Val Ile Leu Ile Glu Leu Glu Lys Ile Glu Asp Tyr Thr Val				
	485		490	495	
	atg cca gag tca att cag tac atc aaa cag aag cat ggt gcc atc cgg				1536
	Met Pro Glu Ser Ile Gln Tyr Ile Lys Gln Lys His Gly Ala Ile Arg				
	500		505	510	
30	tgg cat ggg gac ttc acg gag cag tca cag tgt atg aag acc aag ttt				1584
	Trp His Gly Asp Phe Thr Glu Gln Ser Gln Cys Met Lys Thr Lys Phe				
	515		520	525	
35	tgg aag aca gtg aga tac cac atg ccg ccc aga agg tgt cgg ccg ttt				1632
	Trp Lys Thr Val Arg Tyr His Met Pro Pro Arg Arg Cys Arg Pro Phe				
	530		535	540	
40	ctc ccg tcc acg tgc cgc agc aca cac ctc tgt acc gca ccg cag gcc				1680
	Leu Arg Ser Thr Cys Arg Ser Thr His Leu Cys Thr Ala Pro Gln Ala				
	545		550	555	560
	cag aac tag				1689
45	Gln Asn				
	<210> 13				
	<211> 562				
	<212> PRT				
50	<213> Unknown Organism				
	<223> Description of Unknown Organism: primate; surmised				
	Homo sapiens				
	<400> 13				
55	Met Trp Ser Leu Leu Leu Cys Gly Leu Ser Ile Ala Leu Pro Leu Ser				
	1	5	10	15	
	Val Thr Ala Asp Gly Cys Lys Asp Ile Phe Met Lys Asn Glu Ile Leu				
	20		25	30	
60	Ser Ala Ser Gln Pro Phe Ala Phe Asn Cys Thr Phe Pro Pro Ile Thr				

	35	40	45
	Ser Gly Glu Val Ser Val Thr Trp Tyr Lys Asn Ser Ser Lys Ile Pro		
	50	55	60
5	Val Ser Lys Ile Ile Gln Ser Arg Ile His Gln Asp Glu Thr Trp Ile		
	65	70	75
	80		
10	Leu Phe Leu Pro Met Glu Trp Gly Asp Ser Gly Val Tyr Gln Cys Val		
	85	90	95
	Ile Lys Gly Arg Asp Ser Cys His Arg Ile His Val Asn Leu Thr Val		
	100	105	110
15	Phe Glu Lys His Trp Cys Asp Thr Ser Ile Gly Gly Leu Pro Asn Leu		
	115	120	125
	Ser Asp Glu Tyr Lys Gln Ile Leu His Leu Gly Lys Asp Asp Ser Leu		
	130	135	140
20	Thr Cys His Leu His Phe Pro Lys Ser Cys Val Leu Gly Pro Ile Lys		
	145	150	155
	160		
25	Trp Tyr Lys Asp Cys Asn Glu Ile Lys Gly Glu Arg Phe Thr Val Leu		
	165	170	175
	Glu Thr Arg Leu Leu Val Ser Asn Val Ser Ala Glu Asp Arg Gly Asn		
	180	185	190
30	Tyr Ala Cys Gln Ala Ile Leu Thr His Ser Gly Lys Gln Tyr Glu Val		
	195	200	205
	Leu Asn Gly Ile Thr Val Ser Ile Thr Glu Arg Ala Gly Tyr Gly Gly		
	210	215	220
35	Ser Val Pro Lys Ile Ile Tyr Pro Lys Asn His Ser Ile Glu Val Gln		
	225	230	235
	240		
40	Leu Gly Thr Thr Leu Ile Val Asp Cys Asn Val Thr Asp Thr Lys Asp		
	245	250	255
	Asn Thr Asn Leu Arg Cys Trp Arg Val Asn Asn Thr Leu Val Asp Asp		
	260	265	270
45	Tyr Tyr Asp Glu Ser Lys Arg Ile Arg Glu Gly Val Glu Thr His Val		
	275	280	285
	Ser Phe Arg Glu His Asn Leu Tyr Thr Val Asn Ile Thr Phe Leu Glu		
	290	295	300
50	Val Lys Met Glu Asp Tyr Gly Leu Pro Phe Met Cys His Ala Gly Val		
	305	310	315
	320		
55	Ser Thr Ala Tyr Ile Ile Leu Gln Leu Pro Ala Pro Asp Phe Arg Ala		
	325	330	335
	Tyr Leu Ile Gly Gly Leu Ile Ala Leu Val Ala Val Ala Val Ser Val		
	340	345	350
60	Val Tyr Ile Tyr Asn Ile Phe Lys Ile Asp Ile Val Leu Trp Tyr Arg		
	355	360	365

Ser Ala Phe His Ser Thr Glu Thr Ile Val Asp Gly Lys Leu Tyr Asp
 370 375 380 385 390 395 400
 5 Ala Tyr Val Leu Tyr Pro Lys Pro His Lys Glu Ser Gln Arg His Ala
 385 390 395 400
 Val Asp Ala Leu Val Leu Asn Ile Leu Pro Glu Val Leu Glu Arg Gln
 10 405 410 415
 Cys Gly Tyr Lys Leu Phe Ile Phe Gly Arg Asp Glu Phe Pro Gly Gln
 420 425 430
 15 Ala Val Ala Asn Val Ile Asp Glu Asn Val Lys Leu Cys Arg Arg Leu
 435 440 445
 Ile Val Ile Val Val Pro Glu Ser Leu Gly Phe Gly Leu Leu Lys Asn
 450 455 460
 20 Leu Ser Glu Glu Gln Ile Ala Val Tyr Ser Ala Leu Ile Gln Asp Gly
 465 470 475 480
 Met Lys Val Ile Leu Ile Glu Leu Glu Lys Ile Glu Asp Tyr Thr Val
 25 485 490 495
 Met Pro Glu Ser Ile Gln Tyr Ile Lys Gln Lys His Gly Ala Ile Arg
 500 505 510
 30 Trp His Gly Asp Phe Thr Glu Gln Ser Gln Cys Met Lys Thr Lys Phe
 515 520 525
 Trp Lys Thr Val Arg Tyr His Met Pro Pro Arg Arg Cys Arg Pro Phe
 530 535 540
 35 Leu Arg Ser Thr Cys Arg Ser Thr His Leu Cys Thr Ala Pro Gln Ala
 545 550 555 560
 Gln Asn
 40
 <210> 14
 <211> 1686
 45 <212> DNA
 <213> Unknown Organism
 <220>
 <223> Description of Unknown Organism: rodent; surmised
 50 Rattus sp.
 <220>
 <221> CDS
 <222> (1)..(1683)
 55 <400> 14
 atg ggg atg cca ccc ttg ctc ttc tgt tgg gtg tct ttc gtg ctt cca
 Met Gly Met Pro Pro Leu Leu Phe Cys Trp Val Ser Phe Val Leu Pro
 60 1 5 10 15 48
 ctt ttt gtg gca gca ggt aac tgt act gat gtc tat atg cac cat gag
 96

	Leu Phe Val Ala Ala Gly Asn Cys Thr Asp Val Tyr Met His His Glu					
	20	25	30			
5	atg att tca gag ggc cag cct ttc ccc ttc aac tgc aca tac cct cca Met Ile Ser Glu Gly Gln Pro Phe Pro Phe Asn Cys Thr Tyr Pro Pro	35	40	45	144	
10	gta aca aac ggg gca gtg aat ctg aca tgg cat aga aca ccc agt aag Val Thr Asn Gly Ala Val Asn Leu Thr Trp His Arg Thr Pro Ser Lys	50	55	60	192	
15	agc cca atc tcc atc aac aga cac gtt aga att cac cag gac cag tcc Ser Pro Ile Ser Ile Asn Arg His Val Arg Ile His Gln Asp Gln Ser	65	70	75	80	240
20	tgg att ttg ttt ctt ccg ttg gca ttg gag gac tca ggc atc tat caa Trp Ile Leu Phe Leu Pro Leu Ala Leu Glu Asp Ser Gly Ile Tyr Gln	85	90	95	288	
25	tgt gtt ata aag gat gcc cac agc tgt tac cga ata gct ata aac cta Cys Val Ile Lys Asp Ala His Ser Cys Tyr Arg Ile Ala Ile Asn Leu	100	105	110	336	
30	acc gtt ttt aga aaa cac tgg tgc gac tct tcc aac gaa gag agt tcc Thr Val Phe Arg Lys His Trp Cys Asp Ser Ser Asn Glu Glu Ser Ser	115	120	125	384	
35	ata aat tcc tca gat gag tac cag caa tgg tta ccc ata gga aaa tcg Ile Asn Ser Ser Asp Glu Tyr Gln Trp Leu Pro Ile Gly Lys Ser	130	135	140	432	
40	ggc agt ctg acg tgc cat ctc tac ttc cca gag agc tgt gtt ttg gat Gly Ser Leu Thr Cys His Leu Tyr Phe Pro Glu Ser Cys Val Leu Asp	145	150	155	160	480
45	tca ata aag tgg tat aag ggt tgt gaa gag att aaa gtg agc aag aag Ser Ile Lys Trp Tyr Lys Gly Cys Glu Glu Ile Lys Val Ser Lys Lys	165	170	175	528	
50	ttt tgc cct aca gga aca aag ctt ctt gtt aac aac atc gac gtg gag Phe Cys Pro Thr Gly Thr Lys Leu Leu Val Asn Asn Ile Asp Val Glu	180	185	190	576	
55	gat agt ggg agc tat gca tgc tca gcc aga ctg aca cac ttg ggg aga Asp Ser Gly Ser Tyr Ala Cys Ser Ala Arg Leu Thr His Leu Gly Arg	195	200	205	624	
60	atc ttc acg gtt aga aac tac att gct gtg aat acc aag gaa gtt ggg Ile Phe Thr Val Arg Asn Tyr Ile Ala Val Asn Thr Lys Glu Val Gly	210	215	220	672	
	tct gga gga agg atc cct aac atc acg tat cca aaa aac aac tcc att Ser Gly Gly Arg Ile Pro Asn Ile Thr Tyr Pro Lys Asn Asn Ser Ile	225	230	235	240	720
	gaa gtt caa ctt ggc tcc acc ctc att gtg gac tgc aat ata aca gac Glu Val Gln Leu Gly Ser Thr Leu Ile Val Asp Cys Asn Ile Thr Asp	245	250	255	768	
	acg aag gag aat acg aac ctc aga tgc tgg cga gtt aac aac acc ctg Thr Lys Glu Asn Thr Asn Leu Arg Cys Trp Arg Val Asn Asn Thr Leu				816	

	260	265	270	
5	gtg gac gat tac tac aac gac ttc aaa cgc atc cag gaa gga atc gaa Val Asp Asp Tyr Tyr Asn Asp Phe Lys Arg Ile Gln Glu Gly Ile Glu 275 280 285			864
10	acc aat ctg tct ctg agg aat cac att ctg tac aca gtg aac ata aca Thr Asn Leu Ser Leu Arg Asn His Ile Leu Tyr Thr Val Asn Ile Thr 290 295 300			912
15	ttc tta gaa gtg aaa atg gag gac tac ggc cat cct ttc aca tgc cac Phe Leu Glu Val Lys Met Glu Asp Tyr Gly His Pro Phe Thr Cys His 305 310 315 320			960
20	gct gcg gtg tcc gca gcc tac atc att ctg aaa cgc cca gct cca gac Ala Ala Val Ser Ala Ala Tyr Ile Ile Leu Lys Arg Pro Ala Pro Asp 325 330 335			1008
25	ttc cgg gct tac ctc ata gga ggt ctc atg gct ttc cta ctt ctg gcc Phe Arg Ala Tyr Leu Ile Gly Gly Leu Met Ala Phe Leu Leu Ala 340 345 350			1056
30	gtg tcc att ctg tac atc tac aac acc ttt aag gtc gac atc gtg ctt Val Ser Ile Leu Tyr Ile Tyr Asn Thr Phe Lys Val Asp Ile Val Leu 355 360 365			1104
35	tgg tat agg agt acc ttc cac act gcc cag gct cca gat gac gag aag Trp Tyr Arg Ser Thr Phe His Thr Ala Gln Ala Pro Asp Asp Glu Lys 370 375 380			1152
40	ctg tat gat gcc tat gtc tta tac ccc aag tac cca aga gaa agc cag Leu Tyr Asp Ala Tyr Val Leu Tyr Pro Lys Tyr Pro Arg Glu Ser Gln 385 390 395 400			1200
45	ggc cat gat gtg gac aca ctg gtg ttg aag atc ttg ccc gag gtg ctg Gly His Asp Val Asp Thr Leu Val Leu Lys Ile Leu Pro Glu Val Leu 405 410 415			1248
50	gag aaa cag tgt gga tat aag tta ttc ata ttt ggc agg gat gaa ttc Glu Lys Gln Cys Gly Tyr Lys Leu Phe Ile Phe Gly Arg Asp Glu Phe 420 425 430			1296
55	cct gga caa gct gtg gcc agc gtc att gat gaa aac att aag ctg tgt Pro Gly Gln Ala Val Ala Ser Val Ile Asp Glu Asn Ile Lys Leu Cys 435 440 445			1344
60	agg agg ctg atg gtc ctc gtg gca cca gag aca tcc agc ttc agc ttt Arg Arg Leu Met Val Leu Val Ala Pro Glu Thr Ser Ser Phe Ser Phe 450 455 460			1392
	ctg aag aac ttg act gaa gaa caa atc gct gtc tac aat gcc ctc gtc Leu Lys Asn Leu Thr Glu Glu Gln Ile Ala Val Tyr Asn Ala Leu Val 465 470 475 480			1440
	cag gac ggc atg aag gtc att ctg att gaa ctg gag aga gtc aag gac Gln Asp Gly Met Lys Val Ile Leu Ile Glu Leu Glu Arg Val Lys Asp 485 490 495			1488
	tac agc acc atg ccc gag tcc att cag tac atc cga cag aag cac ggg Tyr Ser Thr Met Pro Glu Ser Ile Gln Tyr Ile Arg Gln Lys His Gly 500 505 510			1536

gcc atc cag tgg gat ggg gac ttc aca gag cag gca cag tgc gcc aag 1584
Ala Ile Gln Trp Asp Gly Asp Phe Thr Glu Gln Ala Gln Cys Ala Lys
515 520 525

5 acg aaa ttc tgg aag aaa gtg aga tat cat atg cca ccc agg agg tac 1632
Thr Lys Phe Trp Lys Lys Val Arg Tyr His Met Pro Pro Arg Arg Tyr
530 535 540

10 ccg gca tct ccc ccc gtc cag ctg cta gga cac aca ccc cgc ata cca 1680
Pro Ala Ser Pro Pro Val Gln Leu Leu Gly His Thr Pro Arg Ile Pro
545 550 555 560

15 ggc tag 1686
Gly

20 <210> 15
<211> 561
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: rodent; surmised
Mus sp.

25 <400> 15
Met Gly Met Pro Pro Leu Leu Phe Cys Trp Val Ser Phe Val Leu Pro
1 5 10 15

30 Leu Phe Val Ala Ala Gly Asn Cys Thr Asp Val Tyr Met His His Glu
20 25 30

Met Ile Ser Glu Gly Gln Pro Phe Pro Phe Asn Cys Thr Tyr Pro Pro
35 40 45

35 Val Thr Asn Gly Ala Val Asn Leu Thr Trp His Arg Thr Pro Ser Lys
50 55 60

40 Ser Pro Ile Ser Ile Asn Arg His Val Arg Ile His Gln Asp Gln Ser
65 70 75 80

45 Trp Ile Leu Phe Leu Pro Leu Ala Leu Glu Asp Ser Gly Ile Tyr Gln
85 90 95

50 Cys Val Ile Lys Asp Ala His Ser Cys Tyr Arg Ile Ala Ile Asn Leu
100 105 110

55 Thr Val Phe Arg Lys His Trp Cys Asp Ser Ser Asn Glu Glu Ser Ser
115 120 125

50 Ile Asn Ser Ser Asp Glu Tyr Gln Gln Trp Leu Pro Ile Gly Lys Ser
130 135 140

55 Gly Ser Leu Thr Cys His Leu Tyr Phe Pro Glu Ser Cys Val Leu Asp
145 150 155 160

55 Ser Ile Lys Trp Tyr Lys Gly Cys Glu Glu Ile Lys Val Ser Lys Lys
165 170 175

60 Phe Cys Pro Thr Gly Thr Lys Leu Leu Val Asn Asn Ile Asp Val Glu
180 185 190

Asp Ser Gly Ser Tyr Ala Cys Ser Ala Arg Leu Thr His Leu Gly Arg
195 200 205

5 Ile Phe Thr Val Arg Asn Tyr Ile Ala Val Asn Thr Lys Glu Val Gly
210 215 220

Ser Gly Gly Arg Ile Pro Asn Ile Thr Tyr Pro Lys Asn Asn Ser Ile
225 230 235 240

10 Glu Val Gln Leu Gly Ser Thr Leu Ile Val Asp Cys Asn Ile Thr Asp
245 250 255

Thr Lys Glu Asn Thr Asn Leu Arg Cys Trp Arg Val Asn Asn Thr Leu
260 265 270

15 Val Asp Asp Tyr Tyr Asn Asp Phe Lys Arg Ile Gln Glu Gly Ile Glu
275 280 285

20 Thr Asn Leu Ser Leu Arg Asn His Ile Leu Tyr Thr Val Asn Ile Thr
290 295 300

Phe Leu Glu Val Lys Met Glu Asp Tyr Gly His Pro Phe Thr Cys His
305 310 315 320

25 Ala Ala Val Ser Ala Ala Tyr Ile Ile Leu Lys Arg Pro Ala Pro Asp
325 330 335

Phe Arg Ala Tyr Leu Ile Gly Gly Leu Met Ala Phe Leu Leu Ala
340 345 350

30 Val Ser Ile Leu Tyr Ile Tyr Asn Thr Phe Lys Val Asp Ile Val Leu
355 360 365

Trp Tyr Arg Ser Thr Phe His Thr Ala Gln Ala Pro Asp Asp Glu Lys
35 370 375 380

385 Leu Tyr Asp Ala Tyr Val Leu Tyr Pro Lys Tyr Pro Arg Glu Ser Gln
390 395 400

40 Gly His Asp Val Asp Thr Leu Val Leu Lys Ile Leu Pro Glu Val Leu
405 410 415

Glu Lys Gln Cys Gly Tyr Lys Leu Phe Ile Phe Gly Arg Asp Glu Phe
420 425 430

45 Pro Gly Gln Ala Val Ala Ser Val Ile Asp Glu Asn Ile Lys Leu Cys
435 440 445

50 Arg Arg Leu Met Val Leu Val Ala Pro Glu Thr Ser Ser Phe Ser Phe
450 455 460

Leu Lys Asn Leu Thr Glu Glu Gln Ile Ala Val Tyr Asn Ala Leu Val
465 470 475 480

55 Gln Asp Gly Met Lys Val Ile Leu Ile Glu Leu Glu Arg Val Lys Asp
485 490 495

Tyr Ser Thr Met Pro Glu Ser Ile Gln Tyr Ile Arg Gln Lys His Gly
500 505 510

60 Ala Ile Gln Trp Asp Gly Asp Phe Thr Glu Gln Ala Gln Cys Ala Lys

DEBETS,

124

DX01073K

515

520

525

Thr Lys Phe Thr Lys Lys Val Arg Tyr His Met Pro Pro Arg Arg Tyr
530 535 540

5

Pro Ala Ser Pro Pro Val Gln Leu Leu Gly His Thr Pro Arg Ile Pro
545 550 555 560

Gly

10